

# SEQUENCE LISTING

<110> Sumitomo Chemical Co., Ltd

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<120> PROCESS FOR PRODUCING OPTICALLY ACTIVE 4-HALO-3-HYDROXYBUTANOATE

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<170> PatentIn Ver. 2.1

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35 tgc acc aag gtg tgg aac cac ctc cac cgt tat gag gac gtc ctc tgg 288  
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   gccctgaaga ccggttaccg tcacttggac tgtgcctggt actacctgaa cgagggtgag 240
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20 aaa gta gtt gtg aac tat cgt tcg aaa gaa gaa gaa gct aac agc gtt 144  
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25 tta gaa gaa att aaa aaa gtg ggc gga gag gct att gcc gtc aaa ggt 192  
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	165 170 175	
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Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg	
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tgc acc aag gtg tgg aac cac ctc cac cgt tat gag gac gtc ctc tgg	288
Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp	
85 90 95	

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Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met	
100 105 110	

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Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu	
115 120 125	

ccc aag att ggc cct gac ggc aaa tac gtc att ctc aag gac ctg acc	432
Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr	
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225 230 235 240

5 gag atc gcc gag aag ggc ggc aac acc ctt gct cag gtt ctt att gcc 768  
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10           tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc   816  
          Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro  
                          260                           265                           270

aag cgc att gag tcc aac ttc aag agc att gag ctc tcc gat gcc gac 864  
Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp  
275 280 285

ttt gaa gcc atc aat gcc gtt gcc aag ggt cgt cac ttc cgt ttc gtc 912  
 Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val  
 290 295 300

20   aac atg aag gat act ttc gga tat gat gtc tgg ccc gag gag acc gcc   960  
Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala  
305                         310                         315                         320

25      aag aac ctg tct gcg tga      978  
       Lys Asn Leu Ser Ala  
               325

30      <210> 31  
         <211> 27  
         <212> DNA  
         <213> Artificial Sequence

35 <220>  
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for PCR

<400> 31  
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$\langle 210 \rangle$	32
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<220>

5 <223> Description of Artificial Sequence Designed oligonucleotide primer  
for PCR

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for PCR

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25

<212> PRT  
<213> Corynebacterium sp.

<400> 34

30 Met Lys Ala Ile Gln Tyr Thr Arg Ile Gly Ala Glu Pro Glu Leu Thr  
1 5 10 15

Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val  
20 25 30

35 Thr Ala Ala Gly Val Cys His Ser Asp Asp Phe Ile Met Ser Leu Pro  
35 40 45

Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Glu Gly  
50 55 60

	Ala Gly Lys Val Ala Ala Val Gly Glu Gly Val Glu Gly Leu Asp Ile	65	70	75	80
5	Gly Thr Asn Val Val Val Tyr Gly Pro Trp Gly Cys Gly Asn Cys Trp	85	90	95	
	His Cys Ser Gln Gly Leu Glu Asn Tyr Cys Ser Arg Ala Gln Glu Leu	100	105	110	
10	Gly Ile Asn Pro Pro Gly Leu Gly Ala Pro Gly Ala Leu Ala Glu Phe	115	120	125	
	Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp	130	135	140	
15	Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His	145	150	155	160
	Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Gly Ser Tyr Ala Val	165	170	175	
	Val Ile Gly Thr Gly Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg	180	185	190	
25	His Leu Ser Ala Ala Thr Val Ile Ala Leu Asp Val Ser Ala Asp Lys	195	200	205	
	Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp	210	215	220	
30	Lys Asp Ala Ala Glu Asn Val Arg Lys Ile Thr Gly Ser Gln Gly Ala	225	230	235	240
	Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala	245	250	255	
	Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly	260	265	270	
40	Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu	275	280	285	

	Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu	
	290	300
5	Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Gly Gly Gly Asp	
	305	320
	Leu Gln Ser Arg Gln Arg Cys Arg Ser Val Ser Thr Thr Gly Cys Arg	
	325	335
10	Asn Ala Gln Arg Pro Cys Gly Cys Gly Pro Trp Ser Val Val Pro Thr	
	340	350
	Ala Val Glu Arg Gln Arg Lys Asn Thr Asp Ala Arg Pro Asn Ser Ile	
15	355	365
	Arg Pro Gly Ile Ser Val Arg Asn Ser Val Cys Ala Ser Cys Thr Pro	
	370	380
20	Arg	
	385	
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25	<211> 1158	
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	Met Lys Ala Ile Gln Tyr Thr Arg Ile Gly Ala Glu Pro Glu Leu Thr	
	1 5 10 15	
	gag att ccc aaa ccc gag ccc ggt cca ggt gaa gtg ctc ctg gaa gtc	96
40	Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val	
	20 25 30	
	acc gct gct ggc gtc tgc cac tcg gac gac ttc atc atg agc ctg ccc	144

	Thr	Ala	Ala	Gly	Val	Cys	His	Ser	Asp	Asp	Phe	Ile	Met	Ser	Leu	Pro	
			35					40					45				
5	gaa	gag	cag	tac	acc	tac	ggc	ctt	ccg	ctc	acg	ctc	ggc	cac	gaa	ggc	192
	Glu	Glu	Gln	Tyr	Thr	Tyr	Gly	Leu	Pro	Leu	Thr	Leu	Gly	His	Glu	Gly	
		50					55					60					
10	gca	ggc	aag	gtc	gcc	gcc	gtc	ggc	gag	ggg	gtc	gaa	ggg	ctc	gac	atc	240
	Ala	Gly	Lys	Val	Ala	Ala	Val	Gly	Glu	Gly	Val	Glu	Gly	Leu	Asp	Ile	
	65					70					75					80	
15	gga	acc	aat	gtc	gtc	gtc	tac	ggg	cct	tgg	ggg	tgc	ggc	aac	tgt	tgg	288
	Gly	Thr	Asn	Val	Val	Val	Tyr	Gly	Pro	Trp	Gly	Cys	Gly	Asn	Cys	Trp	
					85					90					95		
	cac	tgc	tca	caa	gga	ctc	gag	aac	tat	tgc	tct	cgc	gcc	caa	gaa	ctc	336
	His	Cys	Ser	Gln	Gly	Leu	Glu	Asn	Tyr	Cys	Ser	Arg	Ala	Gln	Glu	Leu	
				100					105					110			
20	gga	atc	aat	cct	ccc	ggg	ctc	ggg	gca	ccc	ggc	gcg	ttg	gcc	gag	ttc	384
	Gly	Ile	Asn	Pro	Pro	Gly	Leu	Gly	Ala	Pro	Gly	Ala	Leu	Ala	Glu	Phe	
			115					120					125				
25	atg	atc	gtc	gat	tct	cct	cgc	cac	ctt	gtc	ccg	atc	ggg	gac	ctc	gac	432
	Met	Ile	Val	Asp	Ser	Pro	Arg	His	Leu	Val	Pro	Ile	Gly	Asp	Leu	Asp	
		130					135					140					
30	ccg	gtc	aag	acg	gtg	ccg	ctg	acc	gac	gcc	ggg	ctg	acg	ccg	tat	cac	480
	Pro	Val	Lys	Thr	Val	Pro	Leu	Thr	Asp	Ala	Gly	Leu	Thr	Pro	Tyr	His	
	145					150					155					160	
35	gcg	atc	aag	cgt	tct	ctg	ccg	aaa	ctt	cgc	gga	ggc	tcg	tac	gcg	gtt	528
	Ala	Ile	Lys	Arg	Ser	Leu	Pro	Lys	Leu	Arg	Gly	Gly	Ser	Tyr	Ala	Val	
				165					170					175			
	gtc	att	ggg	acc	ggc	ggg	ctc	ggc	cac	gtc	gct	att	cag	ctc	ctc	cgc	576
	Val	Ile	Gly	Thr	Gly	Gly	Leu	Gly	His	Val	Ala	Ile	Gln	Leu	Leu	Arg	
				180					185					190			
40	cac	ctc	tcg	gcg	gca	acg	gtc	atc	gct	ttg	gac	gtg	agc	gcg	gac	aag	624
	His	Leu	Ser	Ala	Ala	Thr	Val	Ile	Ala	Leu	Asp	Val	Ser	Ala	Asp	Lys	
			195					200					205				

	ctc gaa ctg gca acc aag gta ggc gct cac gaa gtg gtt ctg tcc gac	672
	Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp	
	210 215 220	
5	aag gac gcg gcc gag aac gtc cgc aag atc act gga agt caa ggc gcc	720
	Lys Asp Ala Ala Glu Asn Val Arg Lys Ile Thr Gly Ser Gln Gly Ala	
	225 230 235 240	
10	gca ttg gtt ctc gac ttc gtc ggc tac cag ccc acc atc gac acc gcg	768
	Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala	
	245 250 255	
15	atg gct gtc gcc ggc gtc gga tca gac gtc acg atc gtc ggg atc ggg	816
	Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly	
	260 265 270	
20	gac ggc cag gcc cac gcc aaa gtc ggg ttc ttc caa agt cct tac gag	864
	Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu	
	275 280 285	
25	gct tog gtg aca gtt ccg tat tgg ggt gcc cgc aac gag ttg atc gaa	912
	Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu	
	290 295 300	
30	ttg atc gac ctc gcc cac gcc ggc atc ttc gac atc ggc ggt gga gac	960
	Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Gly Gly Gly Asp	
	305 310 315 320	
35	ott cag tot cga caa cgg tgc cga agc gta tcg acg act ggc tgc cgg	1008
	Leu Gln Ser Arg Gln Arg Cys Arg Ser Val Ser Thr Thr Gly Cys Arg	
	325 330 335	
40	aac gct cag cgg ccg tgc ggt tgt ggt ccc tgg tct gta gta ccg aca	1056
	Asn Ala Gln Arg Pro Cys Gly Cys Gly Pro Trp Ser Val Val Pro Thr	
	340 345 350	
45	gcg gta gaa cga cag cgg aaa aac act gat gcc cgg ccg aat tcg att	1104
	Ala Val Glu Arg Gln Arg Lys Asn Thr Asp Ala Arg Pro Asn Ser Ile	
	355 360 365	
50	cgg ccg ggc atc agt gtc aga aat tcg gtg tgc gct agc tgc acg cct	1152



Arg Pro Gly Ile Ser Val Arg Asn Ser Val Cys Ala Ser Cys Thr Pro  
370 375 380

5 cga tga 1158  
Arg  
385